

Slobodiy

re-run



#22

1600

## RAW SEQUENCE LISTING

DATE: 07/15/2003

PATENT APPLICATION: US/09/830,111D

TIME: 14:08:26

Input Set : N:\Cr4\07092003\I830111D.raw

Output Set: N:\CRF4\07152003\I830111D.raw

1 <110> APPLICANT: Kaneka Corporation  
 2 Matsuda, Hideyuki  
 3 Kawamukai, Makota  
 4 Yajima, Kazuyoshi  
 5 Ikenaka, Yasuhiro  
 6 Hasegawa, Junzo  
 7 Takahashi, Satomi  
 8 <120> TITLE OF INVENTION: Process For Producing Coenzyme Q10  
 9 <130> FILE REFERENCE: 21581-00265-US  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/830,111D  
 11 <141> CURRENT FILING DATE: 2001-07-23  
 12 <160> NUMBER OF SEQ ID NOS: 2  
 13 <170> SOFTWARE: PatentIn version 3.2  
 15 <210> SEQ ID NO: 1  
 16 <211> LENGTH: 1653  
 17 <212> TYPE: DNA  
 18 <213> ORGANISM: Saioella complicata  
 19 <400> SEQUENCE: 1

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22	aaatccatat	accatggcct	caccagcact	gcggatacga	agcatcagct	ctcgatcaat	180
23	cgcctctctg	cgatcggtta	ccctaagaac	agcctcggca	ccttcattac	gactaagatg	240
24	taccccgacg	agccggccat	cgagttcatg	ggctgctgct	gtgtcttcgg	cgtcgagact	300
25	ggttgagcct	gatccgaatc	aacctctcat	caatccgctc	aacttggtcg	gtcccagatg	360
26	gtcaaatctt	acatccaaca	tccgatctct	cctcggttca	ggacaccctt	ctctcgacac	420
27	tgctcgctaaa	tactatgttc	agtctgaggg	aaagcatatt	cgtccgctca	tggtactgct	480
28	gatggctcag	gcgacggagg	ttgcgccaaa	agttcagggg	tgggagaagg	tcgtggagggt	540
29	tccggtgaac	gagggactcg	caccaccaga	gggtctcaat	gacaagaacc	cagatatgat	600
30	gaacatgagg	tcaggaccat	taacgaagga	cggcgagatc	gagggacaga	cgtcgaatat	660
31	cctcgccctcg	caacggcggt	tggctgagat	cacggagatg	atccatgcag	catcactcct	720
32	ccacgacgac	gttatcgacg	cttccgagac	cagacgaaac	gcaccatccg	gaaaccaggc	780
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34	attggcgagg	ttgcgcaatc	cggaggtgat	tgagcttttg	gctactgtta	ttgcaaaact	900
35	ggttgagggg	gagttcatgc	agttgaaaaa	tactgttgat	gatgcgattg	aggctacggc	960
36	gacgcaggaa	acgttcgatt	actatttgca	gaagacttac	ttgaagactg	cgtccttgat	1020
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41	gcgcaagttc	tctgacccag	gagacgtcga	gcgtgcacgc	gagttggctg	agaaaagtga	1320
42	tggattggag	aagacgagag	ccttggcgga	ggagtatgcc	cagaaggcgt	tggatgcaat	1380
43	tcggacgttc	ccggagagtc	cggcacggaa	ggctttggag	cagttgacgg	acaaggtgtt	1440
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45      ggcatgcaag cttggctggt ttggcggatg agagaagatt ttcagcctga tacagattaa      1560
46      atcagaacgc agaagcggtc tgataaaaca gaatttgctt ggcggcagta gcgcggtggt      1620
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53 <400> SEQUENCE: 2
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58      Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser Trp Ala Ala
59      35          40          45
60      Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp Pro Asn Gln Pro
61      50          55          60
62      Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met Ser Asn Leu Thr
63      65          70          75          80
64      Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro Ser Leu Asp Thr
65      85          90          95
66      Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His Ile Arg Pro Leu
67      100         105         110
68      Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala Pro Lys Val Gln
69      115         120         125
70      Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu Gly Leu Ala Pro
71      130         135         140
72      Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met Asn Met Arg Ser
73      145         150         155         160
74      Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln Thr Ser Asn Ile
75      165         170         175
76      Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala
77      180         185         190
78      Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser Glu Thr Arg Arg
79      195         200         205
80      Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys Met Ala Ile Leu
81      210         215         220
82      Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala Leu Ala Arg Leu
83      225         230         235         240
84      Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn Leu
85      245         250         255
86      Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val Asp Asp Ala Ile
87      260         265         270
88      Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr Leu Gln Lys Thr
89      275         280         285
90      Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys Arg Ala Ser Ala
91      290         295         300
92      Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala Ala Tyr Ala Tyr
93      305         310         315         320
94      Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp Asp Met Leu Asp

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95          325          330          335
96 Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala Gly Ala Asp Leu
97          340          345          350
98 Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala Trp Lys His His
99          355          360          365
100 Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser Asp Pro Gly Asp
101          370          375          380
102 Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp Gly Leu Glu Lys
103          385          390          395          400
104 Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile
105          405          410          415
106 Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr
107          420          425          430
108 Asp Lys Val Leu Thr Arg Ser Arg
109          435          440

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**VERIFICATION SUMMARY**

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L:10 M:270 C: Current Application Number differs, Wrong Format